

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/550,985  
Source: TFWP  
Date Processed by STIC: 06/21/2006

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 06/21/2006

PATENT APPLICATION: US/10/550,985

TIME: 10:35:49

Input Set : A:\18744033.APP

Output Set: N:\CRF4\06212006\J550985.raw

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4     EULENBERG, KARSTEN
5     NGUYEN, TRI
6     BURK, ULRIKE
8 <120> TITLE OF INVENTION: USE OF A SECRETED PROTEIN FOR PREVENTING AND TREATING
9     OBESITY, DIABETES AND/OR METABOLIC SYNDROME
11 <130> FILE REFERENCE: 18744-0033
13 <140> CURRENT APPLICATION NUMBER: 10/550,985
14 <141> CURRENT FILING DATE: 2005-09-26
16 <150> PRIOR APPLICATION NUMBER: PCT/EP04/003244
17 <151> PRIOR FILING DATE: 2004-03-26
19 <150> PRIOR APPLICATION NUMBER: EP 03006948.8
20 <151> PRIOR FILING DATE: 2003-03-26
22 <160> NUMBER OF SEQ ID NOS: 7
24 <170> SOFTWARE: PatentIn Ver. 3.3
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27 <211> LENGTH: 2767
28 <212> TYPE: DNA
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34 gctcggcagt gtggtgccag aatgtgaaga cggcgtccga ctgcggggca gtgaagcact 180
35 gcctgcagac cgtttggaac aagccaacag tgaaatccct tccctgcgac atatgcaaag 240
36 acgtttgtcac cgcagctggt gatatgctga aggacaatgc cactgaggag gagatccttg 300
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44 aggagtgtga ccgcctgggc cctggcatgg ccgacatatg caagaactat atcagccagt 780
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47 cctccaagaa tgatcatcct gccctggaac tgggtggagcc cattaagaag cacgaggtcc 960
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50 agctgccgaa gtccctgtcg gaagagtgcc aggaggtggt ggacacgtac ggcagctcca 1140
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52 gctctggcac gcggtgcct gcactgaccg ttcacgtgac tcagccaaag gacggtggct 1260
53 tctgcaagat gtgcaagaag ctggtgggtt atttgatcg caacctggag aaaaacagca 1320
54 ccaagcagga gatcctggct gctcttgaga aaggctgcag cttcctgcca gacccttacc 1380

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56 aggtgatgga tccttccttc gtgtgcttga aaattggagc ctgcccctcg gcccataagc 1500
57 ccttgttggg aactgagaag tgtatatggg gcccaagcta ctggtgccag aacacagaga 1560
58 cagcagccca gtgcaatgct gtcgagcatt gcaaacgcca tgtgtggaac taggaggagg 1620
59 aatattccat cttggcagaa accacagcat tgggtttttt ctacttgtgt gtctggggga 1680
60 atgaacgcac agatctgttt gactttgtta taaaaatagg gctccccac cccccatt 1740
61 tctgtgtcct ttattgtagc attgctgtct gcaagggagc ccctagcccc tagcccctgg 1800
62 cagacatagc tgcttcagtg ccccttttct ctctgctaga tggatgttga tgcactggag 1860
63 gtcttttagc ctgcccttgc atggcgctg ctggaggagg agagagctct gctggcatga 1920
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67 atatgaaaga ttagaagcct ggaataatca ggctttttaa atgatgtaat tcccactgta 2160
68 atagcatagg gattttggaa gcagctgctg gtggcttggg acatcagtgg ggccaagggg 2220
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75 ctgggggtgt ggggggttga agctgtctgt ggccacttg ggcacccacg cttctgtcca 2640
76 cttctggttg ccaggagaca gcaagcaaag ccagcaggac atgaagttgc tattaatagg 2700
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81 &lt;210&gt; SEQ ID NO: 2

82 &lt;211&gt; LENGTH: 524

83 &lt;212&gt; TYPE: PRT

84 &lt;213&gt; ORGANISM: Homo sapiens

86 &lt;400&gt; SEQUENCE: 2

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91 20 25 30
93 Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
94 35 40 45
96 Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
97 50 55 60
99 Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
100 65 70 75 80
102 Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
103 85 90 95
105 Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
106 100 105 110
108 Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
109 115 120 125
111 Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His
112 130 135 140
114 Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro
115 145 150 155 160

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117 Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro
118          165          170          175
120 Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys
121          180          185          190
123 Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile
124          195          200          205
126 Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu
127          210          215          220
129 His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile
130 225          230          235          240
132 Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met
133          245          250          255
135 Met His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp
136          260          265          270
138 Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala
139          275          280          285
141 Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro Ile Lys Lys
142          290          295          300
144 His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe
145 305          310          315          320
147 Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys
148          325          330          335
150 Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser
151          340          345          350
153 Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile
154          355          360          365
156 Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met
157          370          375          380
159 Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val
160 385          390          395          400
162 Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val
163          405          410          415
165 Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile
166          420          425          430
168 Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln
169          435          440          445
171 Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu
172          450          455          460
174 Ile Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly
175 465          470          475          480
177 Ala Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile
178          485          490          495
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181          500          505          510
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184          515          520
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 1146
189 <212> TYPE: DNA

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190 <213> ORGANISM: Homo sapiens
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195 caaagcctgg agcaagcatt gcagtgcaga gccctagggc attgcctaca ggaagtctgg 180
196 ggacatgtgg gagccgatga cctatgccaa gagtgtgagg acatcgtcca catccttaac 240
197 aagatggcca aggaggccat tttccaggac acgatgagga agttcctgga gcaggagtgc 300
198 aacgtcctcc ccttgaagct gctcatgccc cagtgcacc aagtgttga cgactacttc 360
199 cccctgggtca tcgactactt ccagaaccag attgactcaa acggcatctg tatgcacctg 420
200 ggctgtgca aatcccggca gccagagcca gagcaggagc cagggatgtc agaccccctg 480
201 cccaaacctc tgcgggaccc tctgccagac cctctgctgg acaagctcgt cctccctgtg 540
202 ctgcccgggg cctccaggc gaggcctggg cctcacacac aggatctctc cgagcagcaa 600
203 ttccccattc ctctccccta ttgctggctc tgcagggtc tgatcaagcg gatccaagcc 660
204 atgattccca aggggtgcgt acgtgtggca gtggcccagg tgtgccgctg ggtacctctg 720
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206 ctgctggggc gcatgtgtgc ccagctggtc tgccgcctcg tcctccggtg ctccatggat 840
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208 ctctgcatgt ccgtgaccac ccaggccggg aacagcagcg agcaggccat accacaggca 960
209 atgtccagg cctgtgttgg ctccctggctg gacagggaaa agtgcaagca atttgtggag 1020
210 cagcacacgc cccagctgct gaccctgggtg cccaggggct gggatgcca caccacctgc 1080
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212 ctttga 1146
215 <210> SEQ ID NO: 4
216 <211> LENGTH: 381
217 <212> TYPE: PRT
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225 20 25 30
227 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
228 35 40 45
230 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
231 50 55 60
233 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
234 65 70 75 80
236 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
237 85 90 95
239 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
240 100 105 110
242 Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
243 115 120 125
245 Asn Gln Ile Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
246 130 135 140
248 Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
249 145 150 155 160
251 Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
252 165 170 175

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254 Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
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258          195          200          205
260 Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
261          210          215          220
263 Gly Ala Leu Arg Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
264 225          230          235          240
266 Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
267          245          250          255
269 Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
270          260          265          270
272 Leu Val Leu Arg Cys Ser Met Asp Ser Ala Gly Pro Arg Ser Pro
273          275          280          285
275 Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser
276          290          295          300
278 Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala
279 305          310          315          320
281 Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys
282          325          330          335
284 Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg
285          340          345          350
287 Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr
288          355          360          365
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295 <211> LENGTH: 1521
296 <212> TYPE: DNA
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312 gtccatggcc actacttgag tcaaacgggc aggtgcccct agctcctcac agaatcccc 780
313 ctctctgcag agctcctgcg gggggagaag cctcagtgtc tggtcagcag ggacaaaaaa 840
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